

AMENDMENT TO THE SPECIFICATION

Please replace paragraphs [0011] and [0012] with the following amended paragraphs:

[0011] Homologues of LuxR are proteins that share a common evolutionary ancestor with LuxR (as described by Gray, K. M. & Garey, J. R., 2001, Microbiology, 147:2379-2387) and are induced in quorum sensing. Homologues of LuxR are described in PROSITE as being members of the LuxR family of proteins (~~see <http://us.expasy.org/cgi-bin/nicedoc.pl?PS00622>~~). Preferably they are proteins that are found on the outer surface of bacterial membranes during the pre-quorate and quorate phases of bacterial growth and which bind a signalling molecule and are then able to activate transcription. Preferably, they are proteins that share sequence identity with LuxR. Preferably homologues of LuxR share more than 40% sequence identity with LuxR (e.g. more than 50%, 60%, 70%, 80%, 90%, 95%, 99% or more). Preferably homologues of LuxR have residues corresponding to those of LuxR. Preferably homologues of LuxR have residues corresponding to the following residues of LuxR when aligned using the Clustal alignment algorithm (Higgins, D. G., Bleasby, A. J. and Fuchs, R., 1992, CLUSTAL V: improved software for multiple sequence alignment. Computer Applications in the Biosciences (CABIOS), 8(2):189-191): TRP66, TYR70, ASP79, PRO80, GLY121, GLU187 and GLY197. Preferably the homologue of LuxR is selected from the group consisting of AhlR, AhvR, AsaR, BafR, BisR, BpsR, BviR, CarR, CepR, CerR, CinR, CsaR, CviR, EagR, EcbR, EchR, EsaR, ExpR, HalR, LasR, LuxS, M118752, MupR, PcoR, PhzR, PmlR, PpuR, PsmR, PsyR, RaiR, RhiR, RhlR, SdiA, SdiR, SmaR, SolR, SpnR, SprR, SwrR, TraR, TriR, TrlR, TrnR, VanR, VsmR, Y4qH, YenR, YpeR, YpsR, YruR, YtbR and YukR.

[0012] The homologue of LuxR may be a positive regulator (like LuxR) and upregulate expression of certain proteins at high cell density, or may be a negative regulator and upregulate expression expression of certain proteins at low cell density. Examples of negative regulators include SdiA and EsaR (von Bodman et al. 1998 Proc Natl Acad Sci 95(13):7687-92). SdiA homologues are highly conserved, as is demonstrated in Table 1, which shows the output from the Swiss Prot/TrEMBL database (~~see <http://bo.expasy.org/sprot/>~~) when queried with SdiA.

TABLE 1

Sequence	Organism	Identity
P07026	<i>E. coli</i>	100%
Q8XBD0	<i>E. coli</i> 0157: H7	99%
Q7AD11	<i>E. coli</i> 0157: H7	99%
Q8FGM5	<i>E. coli</i> O6	97%
Q83R45	<i>Shigella flexneri</i>	96%
Q7UAB1	<i>Shigella flexneri</i>	96%
Q8Z5T1	<i>Salmonella typhi</i>	72%
Q7CQB6	<i>Salmonella typhimurium</i>	71%
O66040	<i>Salmonella typhimurium</i>	71%